

SEQUENCE LISTING

<110> Simmons, Carl

<120> Maize Defense-Inducible Genes and Their
Use

<130> 1266R

<150> 60/243,120

<151> 2000-10-25

<150> 10/027,559

<151> 2001-10-23

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 459

<212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (0)...(0)

<223> Extensin-like cDNA

<221> CDS

<222> (2)...(253)

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	Gly	Glu	Pro	Pro	Ser	Cys	Ala	Arg	Val	Val	Pro	Ser	Asp	Gly	Asp	Arg	
1					5					10						15	

agg	aac	tgc	ctg	ccc	aac	cgc	ccc	aca	cag	cgc	acg	ccg	cag	cag	tgc		97
Arg	Asn	Cys	Leu	Pro	Asn	Arg	Pro	Thr	Gln	Arg	Thr	Pro	Gln	Gln	Cys		
			20					25					30				

gcc	gcg	ttc	tac	tcg	cag	ccg	ccc	gtc	gac	tgc	gcc	gcg	ttc	cag	tgc		145
Ala	Ala	Phe	Tyr	Ser	Gln	Pro	Pro	Val	Asp	Cys	Ala	Ala	Phe	Gln	Cys		
		35					40					45					

aag	ccg	ttt	gtc	cct	gtt	ccg	ccg	ccg	ccg	ccg	cca	tca	tac	ccc	ggc		193
Lys	Pro	Phe	Val	Pro	Val	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Tyr	Pro	Gly		
	50					55					60						

ccg	ttg	cca	ccg	gta	tac	cct	atg	ccg	tac	gca	tcg	cct	ccg	cca	cct		241
Pro	Leu	Pro	Pro	Val	Tyr	Pro	Met	Pro	Tyr	Ala	Ser	Pro	Pro	Pro	Pro		
65					70					75					80		

gcg	cag	tac	cga	tgattcgtcg	aggagcgaga	agcactatca	ctttcacctt										293
Ala	Gln	Tyr	Arg														

aattcgccac caccgctgct gcgctggatg aagacagcaa agttcaccgt cacaattgta 353
 cgtggtcagt cattgttgtg cttagattag tagtggttctt gattgatagc taccggcata 413
 tagaagatta tattattata cggtgcataa aaaaaaaaaa aaaaaa 459

<210> 2
 <211> 84
 <212> PRT
 <213> Zea mays

<400> 2
 Gly Glu Pro Pro Ser Cys Ala Arg Val Val Pro Ser Asp Gly Asp Arg
 1 5 10 15
 Arg Asn Cys Leu Pro Asn Arg Pro Thr Gln Arg Thr Pro Gln Gln Cys
 20 25 30
 Ala Ala Phe Tyr Ser Gln Pro Pro Val Asp Cys Ala Ala Phe Gln Cys
 35 40 45
 Lys Pro Phe Val Pro Val Pro Pro Pro Pro Pro Ser Tyr Pro Gly
 50 55 60
 Pro Leu Pro Pro Val Tyr Pro Met Pro Tyr Ala Ser Pro Pro Pro Pro
 65 70 75 80
 Ala Gln Tyr Arg

<210> 3
 <211> 597
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> Metallothionin-like cDNA

<221> CDS
 <222> (66)...(302)

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 cgagg atg tct tgc agc tgc gga tca agc tgc aac tgc gga tca agc tgc 110
 Met Ser Cys Ser Cys Gly Ser Ser Cys Asn Cys Gly Ser Ser Cys
 1 5 10 15
 aag tgc ggc aag atg tac cct gac ctg gag gag aag agc ggc ggg ggc 158
 Lys Cys Gly Lys Met Tyr Pro Asp Leu Glu Glu Lys Ser Gly Gly Gly
 20 25 30
 gct cag gcc agc gcc gcc gcc gtc gtc ctc ggc gtt gcc cct gag acg 206
 Ala Gln Ala Ser Ala Ala Ala Val Val Leu Gly Val Ala Pro Glu Thr
 35 40 45
 aag aag gcg gcg cag ttc gag gcg gcg ggc gag tcc ggc gag gcc gct 254
 Lys Lys Ala Ala Gln Phe Glu Ala Ala Gly Glu Ser Gly Glu Ala Ala
 50 55 60
 cac ggc tgc agc tgc ggt gac agc tgc aag tgc agc ccc tgc aac tgc 302
 His Gly Cys Ser Cys Gly Asp Ser Cys Lys Cys Ser Pro Cys Asn Cys
 65 70 75

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tgatcctgct gcgttggttc gtttgcgga tgcattgatg tcaccttttt tttactgtct 362
gctttgtgct tgtggcgtgt caagaataaa ggatggagcc atcgtctggt ctgactctgg 422
ctctccgcca tgcattgctt gtgtcggttc tgttggtgct gtgttggtgc atgtaatcgt 482
atggcatcgt tacacaccat gcattctctga tctctttgcg ccagtgtgtg tgactaagtc 542
cctgtaacga ttggctcaag tgattgaata tatatacaat actgtttttac taaaa 597

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<210> 4
 <211> 79
 <212> PRT
 <213> Zea mays

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<400> 4
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Cys Gly Lys Met Tyr Pro Asp Leu Glu Lys Ser Gly Gly Gly Ala
 20          25          30
Gln Ala Ser Ala Ala Ala Val Val Leu Gly Val Ala Pro Glu Thr Lys
 35          40          45
Lys Ala Ala Gln Phe Glu Ala Ala Gly Glu Ser Gly Glu Ala Ala His
 50          55          60
Gly Cys Ser Cys Gly Asp Ser Cys Lys Cys Ser Pro Cys Asn Cys
 65          70          75

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<210> 5
 <211> 1137
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> Cytosolic Ascorbate Peroxidase-like cDNA

<221> CDS
 <222> (124)...(876)

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tccctcagcc gcgtcgctc gcattctacg atccaaagct ctctctggtc gcaggctcgca 120
gcc atg gcg aag aac tac ccg acc gtg agc gcc gag tac agc gag gct 168
  Met Ala Lys Asn Tyr Pro Thr Val Ser Ala Glu Tyr Ser Glu Ala
    1          5          10          15

gtg gac aag gcc agg cgc aag ctc cga gcc ctc atc gcc gag aag agc 216
Val Asp Lys Ala Arg Arg Lys Leu Arg Ala Leu Ile Ala Glu Lys Ser
    20          25          30

tgc gcc ccg ctc atg ctc cgc ctc gcg tgg cac tcc gcg ggg acg ttc 264
Cys Ala Pro Leu Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe
    35          40          45

gac gtg tcg tcg agg acc gcc ggt cca ttc gcc acg atg aag cat cag 312
Asp Val Ser Ser Arg Thr Gly Gly Pro Phe Gly Thr Met Lys His Gln
    50          55          60

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tcg gaa ttg gct cac ggc gct aac gcg ggg ctg gac atc gcg gtg cgg	360
Ser Glu Leu Ala His Gly Ala Asn Ala Gly Leu Asp Ile Ala Val Arg	
65 70 75	
ctg ctc gag ccc atc aag gag gag ttc cca atc ctc tct tac gcc gat	408
Leu Leu Glu Pro Ile Lys Glu Glu Phe Pro Ile Leu Ser Tyr Ala Asp	
80 85 90 95	
ttc tac cag ctc gcg gga gtt gtg gcc gtg gag gtc acc ggt ggg cct	456
Phe Tyr Gln Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro	
100 105 110	
gag att ccc ttc cac ccc ggt agg gag gac aag cct cag ccc cca cct	504
Glu Ile Pro Phe His Pro Gly Arg Glu Asp Lys Pro Gln Pro Pro Pro	
115 120 125	
gag ggc cgc ctt cct gat gcc act aag ggt tct gac cac ctg agg caa	552
Glu Gly Arg Leu Pro Asp Ala Thr Lys Gly Ser Asp His Leu Arg Gln	
130 135 140	
gtt ttt ggc aag cag atg ggc ttg agc cat cag gac att gtt gcc ctc	600
Val Phe Gly Lys Gln Met Gly Leu Ser His Gln Asp Ile Val Ala Leu	
145 150 155	
tct ggt ggc cac acc ttg gga agg tgc cac aaa gag cgg tct ggt ttc	648
Ser Gly Gly His Thr Leu Gly Arg Cys His Lys Glu Arg Ser Gly Phe	
160 165 170 175	
gag ggg gcc tgg act aca aac cct ttg gtc ttt gac aac tct tac ttc	696
Glu Gly Ala Trp Thr Thr Asn Pro Leu Val Phe Asp Asn Ser Tyr Phe	
180 185 190	
aag gaa ctt ctg agt ggt gat aag gag ggc ctt ttt cag ctc cca agt	744
Lys Glu Leu Leu Ser Gly Asp Lys Glu Gly Leu Phe Gln Leu Pro Ser	
195 200 205	
gac aaa gcc ctg ctg agt gac cct gtc ttc cgc cct ctt gtc gag aaa	792
Asp Lys Ala Leu Leu Ser Asp Pro Val Phe Arg Pro Leu Val Glu Lys	
210 215 220	
tat gct gcg gat gag aag gct ttc ttt gat gac tac aaa gag gcc cac	840
Tyr Ala Ala Asp Glu Lys Ala Phe Phe Asp Asp Tyr Lys Glu Ala His	
225 230 235	
ctc aag ctc tcc gaa ctg ggg ttt gct gat gct taa atagacccta	886
Leu Lys Leu Ser Glu Leu Gly Phe Ala Asp Ala *	
240 245 250	
tcctggagtg atacattctg ctgcatgtgg tcttttgcac ctggagtcaa tgtgaacaag	946
cagattgtcg tattgtcttt ctcgtaataa atttgtcaat gttgagccct taggcttgaa	1006
ttgtgggacc ctttgttcgt tttcctagac tctgatgctg tatgcaactg aaacgagtaa	1066
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aaaaaaaaaa a	1137

<210> 6
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 <212> PRT
 <213> Zea mays

<400> 6
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 Asp Lys Ala Arg Arg Lys Leu Arg Ala Leu Ile Ala Glu Lys Ser Cys
 20 25 30
 Ala Pro Leu Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp
 35 40 45
 Val Ser Ser Arg Thr Gly Gly Pro Phe Gly Thr Met Lys His Gln Ser
 50 55 60
 Glu Leu Ala His Gly Ala Asn Ala Gly Leu Asp Ile Ala Val Arg Leu
 65 70 75 80
 Leu Glu Pro Ile Lys Glu Glu Phe Pro Ile Leu Ser Tyr Ala Asp Phe
 85 90 95
 Tyr Gln Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Glu
 100 105 110
 Ile Pro Phe His Pro Gly Arg Glu Asp Lys Pro Gln Pro Pro Pro Glu
 115 120 125
 Gly Arg Leu Pro Asp Ala Thr Lys Gly Ser Asp His Leu Arg Gln Val
 130 135 140
 Phe Gly Lys Gln Met Gly Leu Ser His Gln Asp Ile Val Ala Leu Ser
 145 150 155 160
 Gly Gly His Thr Leu Gly Arg Cys His Lys Glu Arg Ser Gly Phe Glu
 165 170 175
 Gly Ala Trp Thr Thr Asn Pro Leu Val Phe Asp Asn Ser Tyr Phe Lys
 180 185 190
 Glu Leu Leu Ser Gly Asp Lys Glu Gly Leu Phe Gln Leu Pro Ser Asp
 195 200 205
 Lys Ala Leu Leu Ser Asp Pro Val Phe Arg Pro Leu Val Glu Lys Tyr
 210 215 220
 Ala Ala Asp Glu Lys Ala Phe Phe Asp Asp Tyr Lys Glu Ala His Leu
 225 230 235 240
 Lys Leu Ser Glu Leu Gly Phe Ala Asp Ala
 245 250

<210> 7
 <211> 830
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> Non-specific Lipid Transfer-like cDNA

<221> CDS
 <222> (51)...(386)

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 Met Ala
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gcc acc agc agc aag tcg tcg tcg tcc tcg agc tcg gcg cag cgg gca 104
Ala Thr Ser Ser Lys Ser Ser Ser Ser Ser Ser Ser Ala Gln Arg Ala
      5              10              15

gca gct gcc gcc ctg ctc gtg gcg gtg tcc gtc ctg gtg gtg ggc gcg 152
Ala Ala Ala Ala Leu Leu Val Ala Val Ser Val Leu Val Val Gly Ala
      20              25              30

gcg gcg gtg tgc gac atg agc aac gag cag ttc atg tcg tgc cag ccc 200
Ala Ala Val Cys Asp Met Ser Asn Glu Gln Phe Met Ser Cys Gln Pro
      35              40              45              50

gcg gcg gcc aag acg acg gac ccg ccg gcc gcg ccg tcg cag gcg tgc 248
Ala Ala Ala Lys Thr Thr Asp Pro Pro Ala Ala Pro Ser Gln Ala Cys
      55              60              65

tgc gac gcg ctg gcg ggg gcg gac ctc aag tgc ctg tgc ggc tac aag 296
Cys Asp Ala Leu Ala Gly Ala Asp Leu Lys Cys Leu Cys Gly Tyr Lys
      70              75              80

aac tcg ccg tgg atg ggc gtc tac aac atc gac ccc aag cgc gcc atg 344
Asn Ser Pro Trp Met Gly Val Tyr Asn Ile Asp Pro Lys Arg Ala Met
      85              90              95

gag ctt ccg gcc aag tgc ggc ctc gcc acg ccg ccc gac tgc 386
Glu Leu Pro Ala Lys Cys Gly Leu Ala Thr Pro Pro Asp Cys
      100              105              110

tagcagtgtg ctagccaagc caagccaagc aggaaggccc ccggcattgc tagctgtacg 446
tgtctgtgtg tgcattctgca gcagggtgca ggcagggggc cgtacgtacg tgtctctttc 506
tctctctcat cttgtcaccg tacctatcta gagtgtgtgt gtctgtacta attaaaatgt 566
tcttgctcgtc gtcgtctgtg catgcatgta ccatgtcgtc gtgcatgtct attatgtgtg 626
tgtcgtcgtg tcgatcggtg cgtatagatg cctgtttgtta gcatgtgtgt cattacctag 686
tcgtgtgtag tgtatgtatg tgcttgccgg gcaaaagttg catctagcta aacagtagta 746
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aaaaaaaaaa aaaaaaaaaa aaaa 830

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<210> 8
 <211> 112
 <212> PRT
 <213> Zea mays

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<400> 8
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  1              5              10              15
Arg Ala Ala Ala Ala Ala Leu Leu Val Ala Val Ser Val Leu Val Val
      20              25              30
Gly Ala Ala Ala Val Cys Asp Met Ser Asn Glu Gln Phe Met Ser Cys
      35              40              45
Gln Pro Ala Ala Ala Lys Thr Thr Asp Pro Pro Ala Ala Pro Ser Gln
      50              55              60
Ala Cys Cys Asp Ala Leu Ala Gly Ala Asp Leu Lys Cys Leu Cys Gly
      65              70              75              80
Tyr Lys Asn Ser Pro Trp Met Gly Val Tyr Asn Ile Asp Pro Lys Arg
      85              90              95
Ala Met Glu Leu Pro Ala Lys Cys Gly Leu Ala Thr Pro Pro Asp Cys
      100              105              110

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<210> 9
<211> 678
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (0)...(0)
<223> Proteinase Inhibitor-like cDNA

<221> CDS
<222> (77)...(451)

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ctatactact atcacagtag gaagctagga ggaaaatcaa agcaacaaag ttgccggccg 60
gccgagagaa gcaacc atg aga cct cag gcg tcg tta ctc gtc gtc aca ctg 112
          Met Arg Pro Gln Ala Ser Leu Leu Val Val Thr Leu
                1             5             10

gct gtt atc gtc gtc gtc ctt gca gct ctg cca ctc agc aaa ggg acg 160
Ala Val Ile Val Val Val Leu Ala Ala Leu Pro Leu Ser Lys Gly Thr
          15             20             25

gag gag gaa gga gga ggg gcg gca gtc gcc gcc gtg gac gcc gcc gga 208
Glu Glu Glu Gly Gly Gly Ala Ala Val Ala Ala Val Asp Ala Ala Gly
          30             35             40

acg agc tcg tgg cca tgc tgc gac aag tgt ggt ttc tgc tac gtg tct 256
Thr Ser Ser Trp Pro Cys Cys Asp Lys Cys Gly Phe Cys Tyr Val Ser
          45             50             55             60

gac ccg ccg cag tgc caa tgc ctg gac ttc tcg acg gtc ggg tgc cac 304
Asp Pro Pro Gln Cys Gln Cys Leu Asp Phe Ser Thr Val Gly Cys His
                65             70             75

cca gag tgc aag cag tgc atc agg tac acc gcc gac ggt ggc gtc gac 352
Pro Glu Cys Lys Gln Cys Ile Arg Tyr Thr Ala Asp Gly Gly Val Asp
                80             85             90

atc ccg ccc gtg cac gcc tac cgc tgc gcc gac atc ctc ttc aac ttc 400
Ile Pro Pro Val His Ala Tyr Arg Cys Ala Asp Ile Leu Phe Asn Phe
          95             100             105

tgc gag cgc cgc tgc agt act ccc gcc gca gtt gct gct agc acc aag 448
Cys Glu Arg Arg Cys Ser Thr Pro Ala Ala Val Ala Ala Ser Thr Lys
          110             115             120

tag acggatgcat atgcatgcca tcgttgccgc cgtgtgtgcc gcttcagaga 501
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agaactaaat aaatgttacc gcatgctctt gatgcgtgca tgcctctcct ccttgaataa 561
accaatatatt ctataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 621
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 678

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<210> 10
 <211> 124
 <212> PRT
 <213> Zea mays

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 20 25 30
 Gly Gly Ala Ala Val Ala Ala Val Asp Ala Ala Gly Thr Ser Ser Trp
 35 40 45
 Pro Cys Cys Asp Lys Cys Gly Phe Cys Tyr Val Ser Asp Pro Pro Gln
 50 55 60
 Cys Gln Cys Leu Asp Phe Ser Thr Val Gly Cys His Pro Glu Cys Lys
 65 70 75 80
 Gln Cys Ile Arg Tyr Thr Ala Asp Gly Gly Val Asp Ile Pro Pro Val
 85 90 95
 His Ala Tyr Arg Cys Ala Asp Ile Leu Phe Asn Phe Cys Glu Arg Arg
 100 105 110
 Cys Ser Thr Pro Ala Ala Val Ala Ala Ser Thr Lys
 115 120

<210> 11
 <211> 1281
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> Peroxidase-like cDNA

<221> CDS
 <222> (18)...(1088)

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 Met Thr Thr Arg Cys Cys Leu Val Val Ala Thr
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 ctc ctc gcg gcg ctg ctc tcg gtc agt gcc agc ctc gag ttc ggt ttc 98
 Leu Leu Ala Ala Leu Leu Ser Val Ser Ala Ser Leu Glu Phe Gly Phe
 15 20 25
 tac aac aag acg tgc ccc agc gcc gag acc atc gtg cag cag acc gtg 146
 Tyr Asn Lys Thr Cys Pro Ser Ala Glu Thr Ile Val Gln Gln Thr Val
 30 35 40
 gcc gcc gcg ttc acc aac aac tcc gcc gtc gct ccg gcg ctc ctc cgc 194
 Ala Ala Ala Phe Thr Asn Asn Ser Gly Val Ala Pro Ala Leu Leu Arg
 45 50 55
 atg cac ttc cat gac tgc ttc gtc aga gcc tgc gac gcc tcg gtg ctg 242
 Met His Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu
 60 65 70 75

atc gac tcc acg gcc aac aac aag gcg gag aag gac tcg atc ccc aac	290
Ile Asp Ser Thr Ala Asn Asn Lys Ala Glu Lys Asp Ser Ile Pro Asn	
80 85 90	
agc ccg agc ctg agg ttc ttc gac gtg gtg gac cgc gcc aag gcg tcc	338
Ser Pro Ser Leu Arg Phe Phe Asp Val Val Asp Arg Ala Lys Ala Ser	
95 100 105	
ctg gag gcg cgg tgc ccc ggc gtg gtg tcc tgc gcc gac atc ctc gcc	386
Leu Glu Ala Arg Cys Pro Gly Val Val Ser Cys Ala Asp Ile Leu Ala	
110 115 120	
ttc gcg gcc agg gac agc gtc gtg ctc acc ggc ggc ctc ggc tac aag	434
Phe Ala Ala Arg Asp Ser Val Val Leu Thr Gly Gly Leu Gly Tyr Lys	
125 130 135	
gtg ccg tcc gga cgc cgt gac ggc cgg ata tcc aat gcc acg cag gcc	482
Val Pro Ser Gly Arg Arg Asp Gly Arg Ile Ser Asn Ala Thr Gln Ala	
140 145 150 155	
ctg aac gag ctg ccc ccg ccc ttc ttc aac gcc acc caa ctc gtc gac	530
Leu Asn Glu Leu Pro Pro Pro Phe Phe Asn Ala Thr Gln Leu Val Asp	
160 165 170	
aac ttc gcc tcc aag aac ctc agc ctc gag gac atg gtt gtc ctc tcc	578
Asn Phe Ala Ser Lys Asn Leu Ser Leu Glu Asp Met Val Val Leu Ser	
175 180 185	
ggc gca cac acc atc ggc gtc tcg cac tgc agc agc ttc gcc gga att	626
Gly Ala His Thr Ile Gly Val Ser His Cys Ser Ser Phe Ala Gly Ile	
190 195 200	
aac aac aca ggc gac cgg ctc tac aac ttc agt ggc tca tcc gac ggg	674
Asn Asn Thr Gly Asp Arg Leu Tyr Asn Phe Ser Gly Ser Ser Asp Gly	
205 210 215	
att gat cct gcg ctg agc aaa gcc tac gcg ttc ctc ctc aag agc att	722
Ile Asp Pro Ala Leu Ser Lys Ala Tyr Ala Phe Leu Leu Lys Ser Ile	
220 225 230 235	
tgc ccg tca aac agc ggc cgg ttc ttc ccc aac acg acg acg ttc atg	770
Cys Pro Ser Asn Ser Gly Arg Phe Phe Pro Asn Thr Thr Thr Phe Met	
240 245 250	
gac ctc atc acg ccg gcc aag ttc gac aac aag tac tac gtc ggc ctc	818
Asp Leu Ile Thr Pro Ala Lys Phe Asp Asn Lys Tyr Tyr Val Gly Leu	
255 260 265	
acc aac aac ctg ggc ctc ttc gag tcg gac gcg gcg ctg ctg acc aac	866
Thr Asn Asn Leu Gly Leu Phe Glu Ser Asp Ala Ala Leu Leu Thr Asn	
270 275 280	
gca acc atg aag gcg ctg gtc gac tcc ttc gtg cgc agc gag gcc acg	914
Ala Thr Met Lys Ala Leu Val Asp Ser Phe Val Arg Ser Glu Ala Thr	
285 290 295	
tgg aag acc aag ttc gcc aag tcc atg ctc aag atg ggg cag atc gag	962
Trp Lys Thr Lys Phe Ala Lys Ser Met Leu Lys Met Gly Gln Ile Glu	

300		305		310		315	
gtg ctc acg ggg acg cag ggc gag atc agg cgc aac tgc agg gtc atc							1010
Val Leu Thr Gly Thr Gln Gly Glu Ile Arg Arg Asn Cys Arg Val Ile							
	320			325		330	
aac cct gct aat gcc gcc gcc gac gtc gtc ctt gcc cgt cag cca ggt							1058
Asn Pro Ala Asn Ala Ala Ala Asp Val Val Leu Ala Arg Gln Pro Gly							
	335			340		345	
tca tca gga tcc act gga gtg gct aca agc taaccatatc tcggtgtgtc							1108
Ser Ser Gly Ser Thr Gly Val Ala Thr Ser							
	350			355			
tgcagtgtgt ttggtgtggg atgtgatata gtatatgtca ataactctaga aaactgaaga							1168
agaagcaggt gatgaccaca ctctgtagtg catcacgcgg tgcgtgttca tttaaccgtg							1228
gcgtttgatt gtgaggatga aataaaacac atgtatgacc aaaaaaaaaa aaa							1281

<210> 12
 <211> 357
 <212> PRT
 <213> Zea mays

<400> 12

Met Thr Thr Arg Cys Cys Leu Val Val Ala Thr Leu Leu Ala Ala Leu																
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Leu Ser Val Ser Ala Ser Leu Glu Phe Gly Phe Tyr Asn Lys Thr Cys								25					30			
			20													
Pro Ser Ala Glu Thr Ile Val Gln Gln Thr Val Ala Ala Ala Phe Thr								40				45				
		35														
Asn Asn Ser Gly Val Ala Pro Ala Leu Leu Arg Met His Phe His Asp						55				60						
	50															
Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asp Ser Thr Ala					70					75					80	
65																
Asn Asn Lys Ala Glu Lys Asp Ser Ile Pro Asn Ser Pro Ser Leu Arg				85				90						95		
Phe Phe Asp Val Val Asp Arg Ala Lys Ala Ser Leu Glu Ala Arg Cys								105					110			
		100														
Pro Gly Val Val Ser Cys Ala Asp Ile Leu Ala Phe Ala Ala Arg Asp							120					125				
		115														
Ser Val Val Leu Thr Gly Gly Leu Gly Tyr Lys Val Pro Ser Gly Arg						135					140					
	130															
Arg Asp Gly Arg Ile Ser Asn Ala Thr Gln Ala Leu Asn Glu Leu Pro					150				155						160	
145																
Pro Pro Phe Phe Asn Ala Thr Gln Leu Val Asp Asn Phe Ala Ser Lys					165				170					175		
Asn Leu Ser Leu Glu Asp Met Val Val Leu Ser Gly Ala His Thr Ile							185					190				
		180														
Gly Val Ser His Cys Ser Ser Phe Ala Gly Ile Asn Asn Thr Gly Asp							200				205					
		195														
Arg Leu Tyr Asn Phe Ser Gly Ser Ser Asp Gly Ile Asp Pro Ala Leu						215				220						
	210															
Ser Lys Ala Tyr Ala Phe Leu Leu Lys Ser Ile Cys Pro Ser Asn Ser					230				235						240	
225																
Gly Arg Phe Phe Pro Asn Thr Thr Thr Phe Met Asp Leu Ile Thr Pro					245				250					255		
Ala Lys Phe Asp Asn Lys Tyr Tyr Val Gly Leu Thr Asn Asn Leu Gly							265						270			
		260														

Leu	Phe	Glu	Ser	Asp	Ala	Ala	Leu	Leu	Thr	Asn	Ala	Thr	Met	Lys	Ala
		275					280					285			
Leu	Val	Asp	Ser	Phe	Val	Arg	Ser	Glu	Ala	Thr	Trp	Lys	Thr	Lys	Phe
	290					295					300				
Ala	Lys	Ser	Met	Leu	Lys	Met	Gly	Gln	Ile	Glu	Val	Leu	Thr	Gly	Thr
305					310					315					320
Gln	Gly	Glu	Ile	Arg	Arg	Asn	Cys	Arg	Val	Ile	Asn	Pro	Ala	Asn	Ala
				325					330					335	
Ala	Ala	Asp	Val	Val	Leu	Ala	Arg	Gln	Pro	Gly	Ser	Ser	Gly	Ser	Thr
		340						345					350		
Gly	Val	Ala	Thr	Ser											
		355													

<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<400> 13

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